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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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CORNING INCORPORATED
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EXAMINER	
SMITH, CAROLYN L	
ART UNIT	PAPER NUMBER
1631	

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10/17/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	09/972,469	LAI ET AL.	
	Examiner	Art Unit	
	Carolyn L. Smith	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *27 August 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1,4-12 and 27-34* is/are pending in the application.

4a) Of the above claim(s) *29-34* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1, 4-12, 27-28* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicants' submission, filed 8/27/07, has been entered.

Amended claims 1, 11, and 28, cancelled claims 2-3 and 13-26, filed 8/27/07, are acknowledged. Claims 29-34 remain withdrawn to due being drawn to non-elected subject matter.

Claims herein under examination are 1, 4-12, and 27-28.

Claim Rejections - 35 USC § 112, Second paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1, 4-12, and 27 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 1 (last line) recites "free of polyadenosine sequences" which lacks clarity. It is unclear if Applicants intend these sequences not to have more than two consecutive adenosines or whether these sequences are intended to be made up solely of adenosines. Clarification of this

issue via clearer claim wording is requested. Claims 4-12 and 27 are also rejected due to their dependency from claim 1.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claims 1, 4-10, 12, and 27-28 are rejected under 35 U.S.C. 103(a) as being unpatentable over Keating et al. (P/N 6,274,332) in view of White et al. (US 2001/0024808).

Keating et al. describe a method for amplifying exons (expressed genetic sequences) from human genomic DNA (higher-order eukaryotic species) (abstract; col. 2, lines 42-44; and col. 46, lines 60-62). Keating et al. describe using screening methods to determine if a trapped exon was part of a gene (col. 46, lines 58-59). Keating et al. describe screening alleles after cloning with various techniques including DNA microchip technology (DNA microarray) (col. 12, lines 20-26 and col. 40, lines 11-33). Keating et al. describe identifying a 3' UTR based on the presence of a stop codon and polyadenylation signal in the sequence (Figures 5A-B; stop codon denoted with asterisk; col. 5, paragraph 5). Keating et al. describe identifying polyadenylation signals upstream to the 3'untranslated region with the longest open reading frame being 1654 base pairs of cDNA (col. 47, lines 1-5) which represents a length of at least about 75 nucleotides (instant claim 5), about 200 to 600 bases (instant claim 6), and about 250 to

about 450 bases (instant claim 7), and up to about 2000 nucleotides (instant claim 27). Keating et al. describe using probes to select all or specific regions of KVLQT1 or KCNE1 and screening the whole mRNA (which contains 3'UTR and exons) (col. 21, second and third paragraphs; col. 11, third paragraph; Tables 3 and 8) which encompasses selecting a predetermined sequence within the 3'UTR or exon and designing probes. Keating et al. describe using probes to amplify exons, genomic KCNE1 and cDNA, amplifying a portion of a gene, and providing a set of primers (probes) for amplification of said portion (col. 8, lines 1-26 and 47-55; col. 10, lines 55-58; and col. 21, lines 10-12). Keating et al. describe designing such primers (col. 13, lines 47-49). Keating et al. describe an identification of exons in Figure 2 (col. 5, lines 23-24). Keating et al. describe amplifying genomic samples by PCR using primer pairs (col. 56, lines 39-52). Keating et al. describe amplifying exons on genomic clones, characterizing PCR products, DNA sequencing, and database analyses to reveal 8 exons with similarity to ion channels (col. 46, lines 39-57). Keating et al. describe performing electrophoreses and cutting out SSCP bands (selected predetermined bands) from the gels to be reamplified (second PCR) using the original primer pair, products were separated and DNA was sequenced (col. 56, line 53 to col. 57, line 12) as well as chromatographic techniques (col. 23, third paragraph). The primer pairs listed (col. 56) result in PCR products that do not contain the poly A tail of KCNE1 which represents a product free of polyadenosine sequences. Keating et al. describe that the nucleic acids of their invention possess a sequence with substantial homology with a natural KVLQT1- or KCNE1-encoding gene or a portion thereof (col. 17, lines 1-5). It is noted that the "less than" terminology in instant claims 8 and 9 can include 0%, such that the substantial homology described above represents "homology of less than or equal to about" 40% or 70% as stated in instant claims 8

and 9. It is noted that the terminology "about 20% to 30%" in instant claim 10 can be reasonably and broadly interpreted to be encompassed by the "substantial homology" disclosure as stated above by Keating et al. Keating et al. describe using nucleic acid microchips (col. 40, second paragraph; col. 9, lines 33-60; col. 11, line 60 to col. 12, line 30) including which represents a deposition of sequences on a substrate in an array. Keating et al. describe this method is one of parallel processing at once (col. 12, lines 30-42) which represents a rectilinear format, as stated in instant claim 12. Keating et al. do not describe printing a second PCR product on a substrate to form an array (instant claims 1 and 28) or selecting a sequence by use of computer software (instant claim 4).

White et al. describe using PCR products to create microarrays on nylon fibers (0248) as stated in instant claims 1 and 28. White et al. describe using programs and computer analysis of sequences to rapidly select primers of a predetermined sequence that span do not span more than one exon in the genomic DNA to be used for PCR screening (0223 and 0136) wherein selection of primers of a sequence is a form of selecting the selected sequence, as stated in instant claim 4.

It would have been obvious to one of ordinary skill in the art at the time the invention was made to use computer software in the method of Keating et al. wherein the motivation would have been to rapidly select primers that do not span more than one exon in the genomic DNA which would otherwise complicate the amplification process, as stated by White et al. (0223).

Thus, Keating et al. in view of White et al. make obvious claims 1, 4-10, 12, and 27-28.

Claim 11 is rejected under 35 U.S.C. 103(a) as being unpatentable over Keating et al. (P/N 6,274,332) in view of White et al. (US 2001/0024808) as applied to claims 1, 4-10, 12, and 27-28 above, and further in view of Stoughton et al. (US 2003/0093227).

Keating et al. describe a method for amplifying exons (expressed genetic sequences) from human genomic DNA (higher-order eukaryotic species) (abstract; col. 2, lines 42-44; and col. 46, lines 60-62). Keating et al. describe using screening methods to determine if a trapped exon was part of a gene (col. 46, lines 58-59). Keating et al. describe screening alleles after cloning with various techniques including DNA microchip technology (DNA microarray) (col. 12, lines 20-26 and col. 40, lines 11-33). Keating et al. describe identifying a 3' UTR based on the presence of a stop codon and polyadenylation signal in the sequence (Figures 5A-B; stop codon denoted with asterisk; col. 5, paragraph 5). Keating et al. describe identifying polyadenylation signals upstream to the 3'untranslated region with the longest open reading frame being 1654 base pairs of cDNA (col. 47, lines 1-5) which represents a length of at least about 75 nucleotides (instant claim 5), about 200 to 600 bases (instant claim 6), and about 250 to about 450 bases (instant claim 7), and up to about 2000 nucleotides (instant claim 27). Keating et al. describe using probes to select all or specific regions of KVLQT1 or KCNE1 and screening the whole mRNA (which contains 3'UTR and exons) (col. 21, second and third paragraphs; col. 11, third paragraph; Tables 3 and 8) which encompasses selecting a predetermined sequence within the 3'UTR or exon and designing probes. Keating et al. describe using probes to amplify exons, genomic KCNE1 and cDNA, amplifying a portion of a gene, and providing a set of primers (probes) for amplification of said portion (col. 8, lines 1-26 and 47-55; col. 10, lines 55-58; and col. 21, lines 10-12). Keating et al. describe designing such primers (col. 13, lines 47-

49). Keating et al. describe an identification of exons in Figure 2 (col. 5, lines 23-24). Keating et al. describe amplifying genomic samples by PCR using primer pairs (col. 56, lines 39-52). Keating et al. describe amplifying exons on genomic clones, characterizing PCR products, DNA sequencing, and database analyses to reveal 8 exons with similarity to ion channels (col. 46, lines 39-57). Keating et al. describe performing electrophoreses and cutting out SSCP bands (selected predetermined bands) from the gels to be reamplified (second PCR) using the original primer pair, products were separated and DNA was sequenced (col. 56, line 53 to col. 57, line 12) as well as chromatographic techniques (col. 23, third paragraph). The primer pairs listed (col. 56) result in PCR products that do not contain the poly A tail of KCNE1 which represents a product free of polyadenosine sequences. Keating et al. describe that the nucleic acids of their invention possess a sequence with substantial homology with a natural KVLQT1- or KCNE1-encoding gene or a portion thereof (col. 17, lines 1-5). It is noted that the "less than" terminology in instant claims 8 and 9 can include 0%, such that the substantial homology described above represents "homology of less than or equal to about" 40% or 70% as stated in instant claims 8 and 9. It is noted that the terminology "about 20% to 30%" in instant claim 10 can be reasonably and broadly interpreted to be encompassed by the "substantial homology" disclosure as stated above by Keating et al. Keating et al. describe using nucleic acid microchips (col. 40, second paragraph; col. 9, lines 33-60; col. 11, line 60 to col. 12, line 30) including which represents a deposition of sequences on a substrate in an array. Keating et al. describe this method is one of parallel processing at once (col. 12, lines 30-42) which represents a rectilinear format, as stated in instant claim 12. Keating et al. do not describe printing a second PCR product on a substrate

to form an array (instant claims 1 and 28), selecting a sequence by use of computer software (instant claim 4), or printed product contains over 90% correct sequence (instant claim 11).

White et al. describe using PCR products to create microarrays on nylon fibers (0248) as stated in instant claims 1 and 28. White et al. describe using computer analysis of sequences to rapidly select primers of a predetermined sequence that span do not span more than one exon in the genomic DNA to be used for PCR screening (0223) as stated in instant claims 4. White et al. do not describe a printed product contains over 90% correct sequence (instant claim 11).

Stoughton et al. describe using PCR products of sequences as templates and having a 94% first pass success rate during amplification as well as printing or spotting PCR products on glass slides by a robot (0194), as stated in instant claim 11.

It would have been obvious to one of ordinary skill in the art at the time the invention was made to use computer software in the method of Keating et al. wherein the motivation would have been to rapidly select primers that do not span more than one exon in the genomic DNA which would otherwise complicate the amplification process, as stated by White et al. (0223). It would have been further obvious to have a printed product contain over 90% correct predetermined sequence as stated by Stoughton et al. in the methods of Keating et al. and White et al. wherein the motivation would have been to more accurately obtain comprehensive measurements of gene profiles with perturbations in order to compare and understand the effects of drugs, diagnose disease, and optimize patient drug regimens, as stated by Stoughton et al. (0004-0005, 0009, 0010).

Thus, Keating et al. in view of White et al. and Stoughton et al. make obvious the instant invention.

Applicants summarize Keating et al. Applicants argue that Keating et al. fail to teach amplifying genomic sequences from the 3'UTR regions or printing amplified sequences on a substrate to make DNA arrays. These statements are found unpersuasive as Applicants' claims do not specifically recite amplifying genomic sequences from 3'UTR regions. Furthermore, Keating et al. disclose using probes to select all or specific regions of KVLQT1 or KCNE1 and screening the whole mRNA (which contains 3'UTR and exons) (col. 21, second and third paragraphs; col. 11, third paragraph; Tables 3 and 8) which encompasses selecting a predetermined sequence within the 3'UTR or exon and designing probes. Keating et al. disclose screening alleles after cloning with various techniques including DNA microchip technology (DNA microarray) (col. 12, lines 20-30 and col. 40, lines 11-33). In addition, White et al. describe using PCR products to create microarrays on nylon fibers (0248). Applicants argue that Keating et al. uses preformed DNA microarrays for screening the amplified and sequenced products instead of making an array as recited in the instant claims. This statement is found unpersuasive as White et al. and Stoughton et al. have been added to the 35 USC 103 rejection to address limitations not found in Keating et al. Applicants' arguments are deemed unpersuasive for the reasons given above.

Conclusion

No claim is allowed.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the PTO Fax Center. The faxing of such papers must conform to the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993) (See 37 CFR §1.6(d)). The Central Fax Center number for official correspondence is (571) 273-8300.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Carolyn Smith, whose telephone number is (571) 272-0721. The examiner can normally be reached Monday through Thursday from 8 A.M. to 6:30 P.M.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran, can be reached on (571) 272-0720.

October 12, 2007

/Carolyn Smith/
Primary Examiner
AU 1631